

**INPUT SET: S33187.raw**

**This Raw Listing contains the General  
Information Section and up to the first 5 pages.**

1                           **SEQUENCE LISTING**  
2

## 3     (1)    General Information:

4  
5       (i) APPLICANT: Pelleymounter, Mary Ann  
6                           Hecht, Randy I  
7                           Mann, Michael B**ENTERED**8  
9       (ii) TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS

10      (iii) NUMBER OF SEQUENCES: 6

11      (iv) CORRESPONDENCE ADDRESS:

12       (A) ADDRESSEE: Amgen Inc.  
13       (B) STREET: 1840 Dehavilland Drive  
14       (C) CITY: Thousand Oaks  
15       (D) STATE: California  
16       (E) COUNTRY: U.S.A.  
17       (F) ZIP: 91230-1789

18      (v) COMPUTER READABLE FORM:

19       (A) MEDIUM TYPE: Floppy disk  
20       (B) COMPUTER: IBM PC compatible  
21       (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
22       (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

23      (vi) CURRENT APPLICATION DATA:

24       (A) APPLICATION NUMBER: 09/366,133  
25       (B) FILING DATE:  
26       (C) CLASSIFICATION:

27      (vii) PRIOR APPLICATION DATA:

28       (A) APPLICATION NUMBER: 08/920,608  
29       (B) FILING DATE:

30      (viii) ATTORNEY/AGENT INFORMATION:

31       (A) NAME: Pessin, Karol M.  
32       (C) REFERENCE/DOCKET NUMBER: A-345

33      (2) INFORMATION FOR SEQ ID NO:1:

34       (i) SEQUENCE CHARACTERISTICS:

35       (A) LENGTH: 491 base pairs  
36       (B) TYPE: nucleic acid  
37       (C) STRANDEDNESS: double

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47 (D) TOPOLOGY: linear

48 (ii) MOLECULE TYPE: cDNA

50

51

52

53

54 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

55

56 TCTAGATTG AGTTTAACT TTTAGAAGGA GGAATAACAT ATGGTACCGA TCCAGAAAGT 60

57

58 TCAGGACGAC ACCAAAACCT TAATTAAAAC GATCGTTACG CGTATCAACG ACATCAGTCA 120

59

60 CACCCAGTCG GTCTCCGCTA AACAGCGTGT TACCGGTCTG GACTTCATCC CGGGTCTGCA 180

61

62 CCCGATCCTA AGCTTGTCCA AAATGGACCA GACCCTGGCT GTATACCAGC AGGTGTTAAC 240

63

64 CTCCCTGCCG TCCCAGAACG TTCTTCAGAT CGCTAACGAC CTCGAGAACCT TTCGCGACCT 300

65

66 GCTGCACCTG CTGGCATTCT CCAAATCCTG CTCCCTGCCG CAGACCTCAG GTCTTCAGAA 360

67

68 ACCGGAATCC CTGGACGGGG TCCTGGAAGC ATCCCTGTAC AGCACCGAAG TTGTTGCTCT 420

69

70 GTCCCGTCTG CAGGGTTCCC TTCAGGACAT CCTTCAGCAG CTGGACGTTT CTCCGGAATG 480

71

72 TTAATGGATC C 491

73

74 (2) INFORMATION FOR SEQ ID NO:2:

75

76 (i) SEQUENCE CHARACTERISTICS:

77 (A) LENGTH: 491 base pairs

78 (B) TYPE: nucleic acid

79 (C) STRANDEDNESS: double

80 (D) TOPOLOGY: linear

81

82 (ii) MOLECULE TYPE: cDNA

83

84

85

86

87 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

88

89 AGATCTAAC TCAAAATTGA AAATCTTCCT CCTTATTGTA TACCATGGCT AGGTCTTC 60

90

91 AGTCCTGCTG TGGTTTGGA ATTAATTTCG CTAGCAATGC GCATAGTTGC TGTAGTCAGT 120

92

93 GTGGGTCAAGC CAGAGGCGAT TTGTCGCACA ATGCCAGAC CTGAAGTAGG GCCCAGACGT 180

94

95 GGGCTAGGAT TCGAACAGGT TTTACCTGGT CTGGGACCGA CATATGGTCG TCCACAATTG 240

96

97 GAGGGACGGC AGGGTCTTGC AAGAAGTCTA GCGATTGCTG GAGCTCTGG AAGCGCTGGA 300

98

99 CGACGTGGAC GACCGTAAGA GGTTAGGAC GAGGGACGGC GTCTGGAGTC CAGAAGTCTT 360

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100 TGGCCTTAGG GACCTGCCCG AGGACCTTCG TAGGGACATG TCGTGGCTTC AACAAACGAGA 420  
101  
102 CAGGGCAGAC GTCCCAAGGG AAGTCCTGTA GGAAGTCGTC GACCTGCAAA GAGGCCTTAC 480  
103  
104 AATTACCTAG G 491  
105  
106

107 (2) INFORMATION FOR SEQ ID NO:3:

108  
109 (i) SEQUENCE CHARACTERISTICS:  
110 (A) LENGTH: 147 amino acids  
111 (B) TYPE: amino acid  
112 (C) STRANDEDNESS: single  
113 (D) TOPOLOGY: linear  
114

115 (ii) MOLECULE TYPE: protein  
116  
117  
118  
119

120 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

121  
122 Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys  
123 1 5 10 15  
124  
125 Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser  
126 20 25 30  
127  
128 Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro  
129 35 40 45  
130  
131 Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln  
132 50 55 60  
133  
134 Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile Ala Asn Asp  
135 65 70 75 80  
136  
137 Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser  
138 85 90 95  
139  
140 Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp  
141 100 105 110  
142  
143 Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser  
144 115 120 125  
145  
146 Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser  
147 130 135 140  
148  
149 Pro Glu Cys  
150 145  
151  
152 (2) INFORMATION FOR SEQ ID NO:4:

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153  
154       (i) SEQUENCE CHARACTERISTICS:  
155           (A) LENGTH: 454 base pairs  
156           (B) TYPE: nucleic acid  
157           (C) STRANDEDNESS: double  
158           (D) TOPOLOGY: linear  
159  
160       (ii) MOLECULE TYPE: cDNA  
161  
162  
163  
164  
165       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
166  
167 CATATGGTAC CGATCCAGAA AGTCAGGAC GACACCAAAA CCTTAATTAA AACGATCGTT       60  
168  
169 ACGCGTATCA ACGACATCAG TCACACCCAG TCGGTGAGCT CTAAACAGCG TGTTACAGGC       120  
170  
171 CTGGACTTCA TCCCAGGTCT GCACCCGATC CTGACCTTGT CCAAAATGGA CCAGACCCTG       180  
172  
173 GCTGTATAACC AGCAGATCTT AACCTCCATG CCGTCCCGTA ACAGTTCTTCA GATCTCTAAC       240  
174  
175 GACCTCGAGA ACCTTCGCGA CCTGCTGCAC GTGCTGGCAT TCTCCAAATC CTGCCACCTG       300  
176  
177 CCATGGGCTT CAGGTCTTGA GACTCTGGAC TCTCTGGCG GGGTCCTGGA AGCATCCGGT       360  
178  
179 TACAGCACCG AAGTTGTTGC TCTGTCCCGT CTGCAGGGTT CCCTTCAGGA CATGCTTTGG       420  
180  
181 CAGCTGGACC TGTCTCCGGG TTGTTAATGG ATCC       454  
182  
183       (2) INFORMATION FOR SEQ ID NO:5:  
184  
185       (i) SEQUENCE CHARACTERISTICS:  
186           (A) LENGTH: 454 base pairs  
187           (B) TYPE: nucleic acid  
188           (C) STRANDEDNESS: double  
189           (D) TOPOLOGY: linear  
190  
191       (ii) MOLECULE TYPE: cDNA  
192  
193  
194  
195  
196       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
197  
198 GTATACCATG GCTAGGTCTT TCAAGTCCTG CTGTGGTTTT GGAATTAATT TTGCTAGCAA       60  
199  
200 TGCGCATAGT TGCTGTAGTC AGTGTGGTC AGCCACTCGA GATTTGTCGC ACAATGTCCG       120  
201  
202 GACCTGAAGT AGGGCCCAGA CGTGGGCTAG GACTGGAACA GGTTTTACCT GGTCTGGGAC       180  
203  
204 CGACATATGG TCGTCTAGAA TTGGAGGTAC GGCAGGGCAT TGCAAGAAGT CTAGAGATTG       240  
205

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206 CTGGAGCTCT TGGAAAGCGCT GGACGACGTG CACGACCGTA AGAGGTTTAG GACGGTGGAC 300  
207  
208 GGTACCCGAA GTCCAGAACT CTGAGACCTG AGAGACCCGC CCCAGGACCT TCGTAGGCCA 360  
209  
210 ATGTCGTGGC TTCAACAACG AGACAGGGCA GACGTCCCAA GGGAAAGTCCT GTACGAAACC 420  
211  
212 GTCGACCTGG ACAGAGGCCA AACAAATTACC TAGG 454  
213  
214 (2) INFORMATION FOR SEQ ID NO:6:  
215  
216 (i) SEQUENCE CHARACTERISTICS:  
217 (A) LENGTH: 147 amino acids  
218 (B) TYPE: amino acid  
219 (C) STRANDEDNESS: single  
220 (D) TOPOLOGY: linear  
221  
222 (ii) MOLECULE TYPE: protein  
223  
224  
225  
226  
227 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
228  
229 Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys  
230 1 5 10 15  
231  
232 Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser  
233 20 25 30  
234  
235 Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro  
236 35 40 45  
237  
238 Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln  
239 50 55 60  
240  
241 Ile Leu Thr Ser Met Pro Ser Arg Asn Val Leu Gln Ile Ser Asn Asp  
242 65 70 75 80  
243  
244 Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser  
245 85 90 95  
246  
247 Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly  
248 100 105 110  
249  
250 Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser  
251 115 120 125  
252  
253 Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser  
254 130 135 140  
255  
256 Pro Gly Cys  
257 145  
258

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**SEQUENCE VERIFICATION REPORT  
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Error

Original Text

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**SEQUENCE MISSING ITEM REPORT  
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<< THERE ARE NO ITEMS MISSING >>

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**SEQUENCE CORRECTION REPORT  
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Original Text

Corrected Text